GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 4, 2004, 15:21:50 ; Search time 1.61702 Seconds
(without alignments)
1397.867 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	40	100.0	8	2	AAW32551	Aaw32551 Amyloidog
2	40	100.0	8	4	AAE10663	Aae10663 Human amy
3	40	100.0	8	4	AAE02615	Aae02615 Human amy
4	40	100.0	8	5	ABB78624	Abb78624 Human alp
5	40	100.0	8	6	ABU09765	Abu09765 Amyloidog
6	40	100.0	8	6	ABR61959	Abr61959 Human amy
7	40	100.0	8	7	ABW00134	Abw00134 Beta-amyl
8	40	100.0	9	6	ABU79063	Abu79063 Aggregati
9	40	100.0	9	7	ABW00197	Abw00197 Peptide #

10	40	100.0	10	3	AAY79938	Aay79938 Beta-amyl
11	40	100.0	10	4	AAB46226	Aab46226 Human APP
12	40	100.0	10	4	AAB46228	Aab46228 Human APP
13	40	100.0	10	4	AAB46227	Aab46227 Human APP
14	40	100.0	11	2	AAW32560	Aaw32560 Anti-amyl
15	40	100.0	11	4	AAM52586	Aam52586 Peptide #
16	40	100.0	11	5	AAU99431	Aau99431 Human amy
17	40	100.0	11	5	AAE29504	Aae29504 Amyloid b
18	40	100.0	11	6	ABU79013	Abu79013 Amyloidog
19	40	100.0	11	7	ABW00147	Abw00147 Amyloid-b
20	40	100.0	12	6	AAE35466	Aae35466 Abeta pep
21	40	100.0	13	6	AAE35465	Aae35465 Abeta pep
22	40	100.0	13	6	AAE35467	Aae35467 Abeta pep
23	40	100.0	13	6	ADA37467	Ada37467 Human amy
24	40	100.0	14	6	ADA89887	Ada89887 Beta-A4 s
25	40	100.0	15	2	AAW02334	Aaw02334 Beta-amyl
26	40	100.0	15	2	AAW89358	Aaw89358 Beta-amyl
27	40	100.0	15	2	AAW89354	Aaw89354 Beta-amyl
28	40	100.0	15	5	ABG71014	Abg71014 Long form
29	40	100.0	15	5	ABB05162	Abb05162 Beta amyl
30	40	100.0	15	5	AAE26271	Aae26271 Human bet
31	40	100.0	15	6	ABU79057	Abu79057 Aggregati
32	40	100.0	15	6	ABU79064	Abu79064 Aggregati
33	40	100.0	15	6	ABU79055	Abu79055 Aggregati
34	40	100.0	15	6	ABU79056	Abu79056 Aggregati
35	40	100.0	15	6	ABU79062	Abu79062 Aggregati
36	40	100.0	15	7	ABW00190	Abw00190 Peptide #
37	40	100.0	15	7	ABW00198	Abw00198 Peptide #
38	40	100.0	15	7	ABW00189	Abw00189 Peptide #
39	40	100.0	15	7	ABW00191	Abw00191 Peptide #
40	40	100.0	15	7	ABW00196	Abw00196 Peptide #
41	40	100.0	16	5	AAE26330	Aae26330 Human bet
42	40	100.0	17	2	AAR54703	Aar54703 Beta-amyl
43	40	100.0	17	2	AAW18880	Aaw18880 Beta-amyl
44	40	100.0	17	4	AAB91774	Aab91774 Amyloid b
45	40	100.0	17	4	AAB91807	Aab91807 Amyloid b

ALIGNMENTS

RESULT 1
AAW32551
ID AAW32551 standard; peptide; 8 AA.
XX
AC AAW32551;
XX
DT 21-JAN-1998 (first entry)
XX
DE Amyloidogenic sequence amyloid beta-peptide.
XX
KW Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW prion associated human neurodegenerative disease; scrapie;
KW spongiform encephalopathy; transmissible mink encephalopathy;

KW chronic wasting disease; mule; deer; elk; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9639834-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US010220.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 1997-051637/05.
XX
PT New inhibitors of fibrillogenesis proteins or peptides - used for
PT preventing, treating or detecting amyloidosis disorders such as
PT Alzheimer's disease.
XX
PS Disclosure; Fig 1A; 63pp; English.
XX
CC A method has been developed for the prevention or treatment of a disorder
CC or disease associated with the formation of amyloid or amyloid-like
CC deposits, involving the abnormal folding of a protein or peptide. The
CC method involves administering an inhibitory peptide which prevents the
CC abnormal folding or which dissolves existing amyloid or amyloid-like
CC deposits, where the peptide comprises a sequence of 3-15 amino acid
CC residues and has a hydrophobic cluster of at least 3 amino acids, where
CC at least one of the 3 amino acids is a beta-sheet blocking amino acid
CC residue selected from Pro, Gly, Asn and His. The present sequence
CC represents an amyloidogenic sequence, amyloid beta- peptide, which is
CC involved in the formation of several amyloid deposits. The inhibitory
CC peptide is capable of associating with a structural determinant on the
CC protein or peptide to structurally block and inhibit the abnormal folding
CC into amyloid or amyloid-like deposits. The method can be used for
CC preventing, treating or detecting e.g. Alzheimer's dementia or disease,
CC Down's syndrome, other amyloidosis disorders, human prion diseases such
CC as Kuru, Creutzfeldt-Jakob disease, Gerstmann- Straussler-Scheinker
CC Syndrome, prion associated human neurodegenerative diseases or animal
CC prion diseases such as scrapie, spongiform encephalopathy, transmissible
CC mink encephalopathy and chronic wasting disease of mule deer and elk
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
    ||||||||
Db 1 KLVFFAED 8

RESULT 2
AAE10663
ID AAE10663 standard; peptide; 8 AA.
XX
AC AAE10663;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KW alpha-secretase.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Cleavage-site   4. .5
XX
PN GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-00023315.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2001-444208/48.
XX
PT Polypeptide comprising fragments of human aspartyl protease with amyloid
PT precursor protein processing activity and alpha-secretase activity, for
PT identifying modulators useful in treating Alzheimer's disease.
XX
PS Claim 10; Page 163; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
CC proteins which lack transmembrane domain or amino terminal domain or
CC cytoplasmic domain and retains alpha-secretase activity and amyloid
CC protein precursor (APP) processing activity. The proteins of the
CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
CC are useful for treating Alzheimer's disease (AD) which causes progressive
CC dementia with consequent formation of amyloid plaques, neurofibrillary
CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
CC with the substrate under acidic conditions and determining the level of

CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC precursor protein (APP) substrate alpha-secretase peptide which is used
CC for determining the enzymatic activity of Asp-1 protein lacking
CC transmembrane domain (TM) and containing a (His)6 tag
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 3
AAE02615
ID AAE02615 standard; peptide; 8 AA.
XX
AC AAE02615;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human amyloid precursor protein substrate alpha-secretase peptide #2.
XX
KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
KW beta-secretase.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 4. .5
XX
PN WO200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US026080.
XX
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI; 2001-290516/30.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Claim 10; Page 98; 189pp; English.
XX

CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human amyloid precursor
CC protein (APP) substrate alpha-secretase peptide which is used for
CC determining the enzymatic activity of Asp-1 deltaTM (His)6 protein
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 4
ABB78624
ID ABB78624 standard; peptide; 8 AA.
XX
AC ABB78624;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human alpha secretase (Abeta12-28) peptide SEQ ID NO:73.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease; proteolytic.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-00025934.
XX
PR 23-SEP-1999; 99US-00404133.
PR 23-SEP-1999; 99US-0155493P.
PR 23-SEP-1999; 99WO-US020881.
PR 13-OCT-1999; 99US-00416901.
PR 06-DEC-1999; 99US-0169232P.
PR 22-SEP-2000; 2000GB-00023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowkski MJ, Gurney M;
XX
DR WPI; 2002-397167/43.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect aspartyl
PT protease activity, e.g. for the diagnosis of Alzheimer's disease.
XX
PS Example 15; Page 92; 182pp; English.

XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)
CC substrate (I) which comprises a peptide of no more than 50 amino acids,
CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
CC (I) under acidic conditions; and (b) determining the level of hu-Asp1
CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
CC nucleotide sequence that hybridises under stringent conditions to the non
CC -coding strand complementary to a defined 1804 nucleotide sequence (see
CC ABL52456) where the nucleotide sequence encodes a polypeptide having Asp1
CC proteolytic activity and lacks nucleotides encoding a transmembrane
CC domain); (3) a purified polynucleotide (III') comprising a sequence that
CC hybridises under stringent conditions to (III) (the nucleotide sequence
CC encodes a polypeptide further lacking a pro-peptide domain corresponding
CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
CC comprising (III) or (III'); and (5) a host cell (V) transformed or
CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
CC substrate (I) may be used as an enzyme substrate in assays to detect
CC aspartyl protease activity, (II) and therefore diagnose diseases
CC associated with aberrant hu-Asp1 expression and activity such as
CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
CC sequence represents a human alpha secretase peptide, which is used in an
CC example from the present invention
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8
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RESULT 5
ABU09765
ID ABU09765 standard; peptide; 8 AA.
XX
AC ABU09765;
XX
DT 17-JUN-2003 (first entry)
XX
DE Amyloidogenic Amyloid beta-peptide #1.
XX
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.
XX
OS Homo sapiens.
XX

PN US6462171-B1.
XX
PD 08-OCT-2002.
XX
PF 12-DEC-1996; 96US-00766596.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-379012/36.
XX
PT Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.
XX
PS Example 1; Fig 1A; 51pp; English.
XX
CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as
CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
    ||||||||
Db 1 KLVFFAED 8

RESULT 6
ABR61959
ID ABR61959 standard; protein; 8 AA.
XX
AC ABR61959;

XX
DT 12-SEP-2003 (first entry)
XX
DE Human amyloid precursor protein (APP) fragment.
XX
KW Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;
KW beta-amyloid protein; Alzheimer's disease; amyloid precursor protein;
KW APP; human.
XX
OS Homo sapiens.
XX
PN WO2003039454-A2.
XX
PD 15-MAY-2003.
XX
PF 23-OCT-2002; 2002WO-US034324.
XX
PR 23-OCT-2001; 2001US-0335952P.
PR 27-NOV-2001; 2001US-0333545P.
PR 14-JAN-2002; 2002US-0348464P.
PR 14-JAN-2002; 2002US-0348615P.
PR 20-JUN-2002; 2002US-0390804P.
PR 19-JUL-2002; 2002US-0397557P.
PR 19-JUL-2002; 2002US-0397619P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII) UNIV ILLINOIS FOUND.
XX
PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;
PI Turner RT;
XX
DR WPI; 2003-541410/51.
XX
PT New peptide compounds are memapsin beta secretase inhibitors used for
PT treating Alzheimer's disease.
XX
PS Example 2; Page 156; 407pp; English.
XX
CC The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a human amyloid precursor protein (APP)
CC fragment where hydolysis by memapsin takes place
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 40; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 7

ABW00134
ID ABW00134 standard; peptide; 8 AA.
XX
AC ABW00134;
XX
DT 15-JAN-2004 (first entry)
XX
DE Beta-amyloid peptide.
XX
KW Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
KW Alzheimer's disease; beta-amyloid.
XX
OS Unidentified.
XX
PN US2003087407-A1.
XX
PD 08-MAY-2003.
XX
PF 06-SEP-2002; 2002US-00235483.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
PR 12-DEC-1996; 96US-00766596.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-616149/58.
XX
PT New inhibitory peptide, useful for preparing a composition for
PT diagnosing, preventing or treating disorders associated with amyloid-like
PT fibril deposits, e.g. Alzheimer's disease, or prion related
PT encephalopathies.
XX
PS Example 1; Fig 1A; 52pp; English.
XX
CC The invention relates to inhibitory peptide comprising a portion of at
CC least three amino acid residues and a sequence predicted not to adopt a
CC beta-sheet structure that associates with a hydrophobic beta-sheet
CC cluster on a protein or peptide involved in the abnormal folding into a
CC beta-sheet structure, to structurally block the abnormal folding of the
CC protein or peptide. The inhibitory peptide is useful for preparing a
CC composition for preventing, treating or detecting disorders or diseases
CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
CC prion related encephalopathies. The invention is also useful in gene
CC therapy. The present sequence is beta-amyloid peptide. This peptide is
CC involved in the formation of several amyloid deposits
XX
SQ Sequence 8 AA;

  Query Match   100.0%; Score 40; DB 7; Length 8;
  Best Local Similarity   100.0%; Pred. No. 1.4e+06;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||

Db 1 KLVFFAED 8

RESULT 8
ABU79063
ID ABU79063 standard; peptide; 9 AA.
XX
AC ABU79063;
XX
DT 17-JUN-2003 (first entry)
XX
DE Aggregation blocking peptide #15.
XX
KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KW pathological beta-sheet-rich conformation; Down's syndrome;
KW amyloidosis disorder; human prion disease; kuru; CJD;
KW Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker syndrome; GSS;
KW prion associated human neurodegenerative disease; animal prion disease;
KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease.
XX
OS Unidentified.
XX
PN US6462171-B1.
XX
PD 08-OCT-2002.
XX
PF 12-DEC-1996; 96US-00766596.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-379012/36.
XX
PT Novel inhibitory peptides which inhibit and structurally block abnormal
PT folding of protein into amyloid or amyloid-like deposit and into
PT pathological beta-sheet rich conformation, useful for treating
PT Alzheimer's disease.
XX
PS Disclosure; Col 51-52; 51pp; English.
XX
CC The invention describes an isolated inhibitory peptide (I) which
CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC residues on a protein or peptide for amyloid or amyloid-like deposit
CC formation, and inhibits or structurally blocks the abnormal folding of
CC proteins and peptides into amyloid or amyloid-like deposits and into
CC pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC diseases associated with abnormal protein folding into amyloid or amyloid
CC -like deposits or into pathological beta-sheet-rich precursors of such
CC deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC (CJD), Gerstmann-Straussler-Scheinker syndrome (GSS), prion associated
CC human neurodegenerative diseases as well as animal prion diseases such as

CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC chronic wasting disease of mule deer and elk. (I) is also useful for
CC detecting and diagnosing the presence or absence of amyloid or amyloid-
CC like deposits in vivo and its precursors. This is the amino acid sequence
CC of peptide associated with the inhibition of amyloid or amyloid like
CC deposits
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9
```

RESULT 9
ABW00197
ID ABW00197 standard; peptide; 9 AA.
XX
AC ABW00197;
XX
DT 15-JAN-2004 (first entry)
XX
DE Peptide #15 used in the invention.
XX
KW Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
KW Alzheimer's disease.
XX
OS Unidentified.
XX
PN US2003087407-A1.
XX
PD 08-MAY-2003.
XX
PF 06-SEP-2002; 2002US-00235483.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
PR 12-DEC-1996; 96US-00766596.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 2003-616149/58.
XX
PT New inhibitory peptide, useful for preparing a composition for
PT diagnosing, preventing or treating disorders associated with amyloid-like
PT fibril deposits, e.g. Alzheimer's disease, or prion related
PT encephalopathies.
XX
PS Claim 1; Page 28; 52pp; English.
XX
CC The invention relates to inhibitory peptide comprising a portion of at

CC least three amino acid residues and a sequence predicted not to adopt a
CC beta-sheet structure that associates with a hydrophobic beta-sheet
CC cluster on a protein or peptide involved in the abnormal folding into a
CC beta-sheet structure, to structurally block the abnormal folding of the
CC protein or peptide. The inhibitory peptide is useful for preparing a
CC composition for preventing, treating or detecting disorders or diseases
CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
CC prion related encephalopathies. The invention is also useful in gene
CC therapy. The present sequence is a peptide used in the invention
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9
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RESULT 10
AAY79938
ID AAY79938 standard; peptide; 10 AA.
XX
AC AAY79938;
XX
DT 11-MAY-2000 (first entry)
XX
DE Beta-amyloid recognition peptide SEQ ID NO:3.
XX
KW Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
KW Alzheimer's disease; neuroprotective; nootropic.
XX
OS Homo sapiens.
XX
PN US6022859-A.
XX
PD 08-FEB-2000.
XX
PF 14-NOV-1997; 97US-00970833.
XX
PR 15-NOV-1996; 96US-0030840P.
XX
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Murphy RM, Kiessling LL;
XX
DR WPI; 2000-160387/14.
XX
PT Beta-amyloid inhibitor useful for treating Alzheimer's disease.
XX
PS Example; Col 7; 15pp; English.
XX
CC The present invention describes a beta-amyloid inhibitor peptide. Beta-
CC amyloid inhibitors have neuroprotective and nootropic properties. The
CC inhibitor peptides are useful for the treatment of Alzheimer's disease.

CC The present sequence represents a beta-amyloid recognition peptide used
CC in the exemplification of present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8
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RESULT 11
AAB46226
ID AAB46226 standard; peptide; 10 AA.
XX
AC AAB46226;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #22.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.
XX
PS Disclosure; Fig 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 3 KLVFFAED 10

RESULT 12
AAB46228
ID AAB46228 standard; peptide; 10 AA.
XX
AC AAB46228;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #24.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.
XX
PS Disclosure; Fig 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
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Db          1 KLVFFAED 8
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RESULT 13
AAB46227
ID AAB46227 standard; peptide; 10 AA.
XX
AC AAB46227;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #23.
XX
KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KW amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014810.
XX
PR 28-MAY-1999; 99US-00322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.
XX
PS Disclosure; Fig 19; 143pp; English.

XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9
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RESULT 14
AAW32560
ID AAW32560 standard; peptide; 11 AA.
XX
AC AAW32560;
XX
DT 21-JAN-1998 (first entry)
XX
DE Anti-amyloid peptide Abeta inhibiting abnormal protein folding.
XX
KW Anti-amyloid peptide; iAbeta; abnormal protein folding inhibitor;
KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
KW Gerstmann-Straussler-Scheinker Syndrome; animal prion disease;
KW prion associated human neurodegenerative disease; scrapie;
KW spongiform encephalopathy; transmissible mink encephalopathy;
KW chronic wasting disease; mule; deer; elk; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9639834-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US010220.
XX
PR 07-JUN-1995; 95US-00478326.
PR 10-APR-1996; 96US-00630645.
XX
PA (UYNY) UNIV NEW YORK STATE.

XX
PI Soto-Jara C, Baumann MH, Frangione B;
XX
DR WPI; 1997-051637/05.
XX
PT New inhibitors of fibrillogenesis proteins or peptides - used for
PT preventing, treating or detecting amyloidosis disorders such as
PT Alzheimer's disease.
XX
PS Example 1; Fig 9; 63pp; English.
XX
CC A method has been developed for the prevention or treatment of a disorder
CC or disease associated with the formation of amyloid or amyloid-like
CC deposits, involving the abnormal folding of a protein or peptide. The
CC method involves administering an inhibitory peptide which prevents the
CC abnormal folding or which dissolves existing amyloid or amyloid-like
CC deposits, where the peptide comprises a sequence of 3-15 amino acid
CC residues and has a hydrophobic cluster of at least 3 amino acids, where
CC at least one of the 3 amino acids is a beta-sheet blocking amino acid
CC residue selected from Pro, Gly, Asn and His. The present sequence
CC represents an anti-amyloid peptide, Abeta, which inhibits abnormal
CC protein folding. The inhibitory peptide is capable of associating with a
CC structural determinant on the protein or peptide to structurally block
CC and inhibit the abnormal folding into amyloid or amyloid-like deposits.
CC The method can be used for preventing, treating or detecting e.g.
CC Alzheimer's dementia or disease, Down's syndrome, other amyloidosis
CC disorders, human prion diseases such as Kuru, Creutzfeldt-Jakob disease,
CC Gerstmann-Straussler-Scheinker Syndrome, prion associated human
CC neurodegenerative diseases or animal prion diseases such as scrapie,
CC spongiform encephalopathy, transmissible mink encephalopathy and chronic
CC wasting disease of mule deer and elk
XX
SQ Sequence 11 AA;

  Query Match   100.0%; Score 40; DB 2; Length 11;
  Best Local Similarity   100.0%; Pred. No. 0.044;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   2 KLVFFAED 9

RESULT 15
AAM52586
ID AAM52586 standard; peptide; 11 AA.
XX
AC AAM52586;
XX
DT 07-FEB-2002 (first entry)
XX
DE Peptide #16 for illustrating method of anticipating protein interaction.
XX
KW Protein interaction; biochemistry; molecular biology; drug development;
KW agrochemical; bioengineering.
XX
OS Unidentified.

XX
PN WO200167299-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-JP001846.
XX
PR 10-MAR-2000; 2000JP-00072485.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
PA (FUIT) FUJITSU LTD.
XX
PI Doi H, Suzuki A;
XX
DR WPI; 2001-570799/64.
XX
PT Method for assaying a specific protein for assaying anticipated
PT information.
XX
PS Example 14; Page 34; 64pp; Japanese.
XX
CC The present invention relates to a method for anticipating interaction
CC between proteins. The method comprises (1) digesting protein A into
CC oligopeptides; (2) searching a protein sequence database for polypeptides
CC (polypeptide C) containing these oligopeptide sequences or D their
CC homologues; (3) performing a local alignment of A and detected C or D;
CC and (4) using a value calculated from the amino acid or oligonucleotide
CC frequencies, anticipating that C or D is polypeptide B that interacts
CC with A. The method is useful for assaying anticipated information about
CC proteins in biochemical, molecular biology, drug development,
CC agrochemical and bioengineering areas. The present sequence was used to
CC illustrate the method
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 40; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8
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Job time : 2.61702 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:31:20 ; Search time 0.519149 Seconds
(without alignments)
795.548 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	8	2	US-08-630-645-1	Sequence 1, Appli
2	40	100.0	8	4	US-08-766-596A-1	Sequence 1, Appli
3	40	100.0	8	5	PCT-US96-10220-1	Sequence 1, Appli
4	40	100.0	9	4	US-08-766-596A-64	Sequence 64, Appl
5	40	100.0	10	3	US-08-970-833-3	Sequence 3, Appli
6	40	100.0	11	2	US-08-630-645-14	Sequence 14, Appl
7	40	100.0	11	4	US-08-766-596A-14	Sequence 14, Appl
8	40	100.0	11	5	PCT-US96-10220-14	Sequence 14, Appl
9	40	100.0	14	4	US-09-594-366-5	Sequence 5, Appli
10	40	100.0	15	2	US-08-612-785B-14	Sequence 14, Appl
11	40	100.0	15	2	US-08-612-785B-37	Sequence 37, Appl

12	40	100.0	15	4	US-08-617-267C-14	Sequence 14, Appl
13	40	100.0	15	4	US-08-766-596A-56	Sequence 56, Appl
14	40	100.0	15	4	US-08-766-596A-57	Sequence 57, Appl
15	40	100.0	15	4	US-08-766-596A-58	Sequence 58, Appl
16	40	100.0	15	4	US-08-766-596A-63	Sequence 63, Appl
17	40	100.0	15	4	US-08-766-596A-65	Sequence 65, Appl
18	40	100.0	17	4	US-09-264-709A-2	Sequence 2, Appli
19	40	100.0	17	4	US-09-594-366-3	Sequence 3, Appli
20	40	100.0	19	3	US-08-970-833-11	Sequence 11, Appl
21	40	100.0	20	3	US-08-970-833-10	Sequence 10, Appl
22	40	100.0	26	1	US-08-304-585-7	Sequence 7, Appli
23	40	100.0	28	1	US-08-346-849-4	Sequence 4, Appli
24	40	100.0	28	1	US-08-302-808-7	Sequence 7, Appli
25	40	100.0	28	2	US-08-609-090-2	Sequence 2, Appli
26	40	100.0	28	2	US-08-986-948-7	Sequence 7, Appli
27	40	100.0	28	2	US-08-293-284A-4	Sequence 4, Appli
28	40	100.0	28	2	US-08-461-216-2	Sequence 2, Appli
29	40	100.0	28	3	US-09-388-890-2	Sequence 2, Appli
30	40	100.0	28	3	US-09-388-890-3	Sequence 3, Appli
31	40	100.0	28	3	US-09-388-890-4	Sequence 4, Appli
32	40	100.0	28	3	US-09-388-890-5	Sequence 5, Appli
33	40	100.0	28	3	US-09-388-890-6	Sequence 6, Appli
34	40	100.0	28	3	US-09-388-890-7	Sequence 7, Appli
35	40	100.0	28	3	US-09-388-890-8	Sequence 8, Appli
36	40	100.0	28	3	US-09-388-890-9	Sequence 9, Appli
37	40	100.0	28	3	US-09-388-890-10	Sequence 10, Appl
38	40	100.0	28	3	US-09-388-890-14	Sequence 14, Appl
39	40	100.0	28	4	US-09-264-709A-1	Sequence 1, Appli
40	40	100.0	28	4	US-08-723-661B-2	Sequence 2, Appli
41	40	100.0	28	4	US-09-660-954-2	Sequence 2, Appli
42	40	100.0	28	4	US-09-660-954-3	Sequence 3, Appli
43	40	100.0	28	4	US-09-660-954-4	Sequence 4, Appli
44	40	100.0	28	4	US-09-660-954-5	Sequence 5, Appli
45	40	100.0	28	4	US-09-660-954-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington

```
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/630,645
;       FILING DATE:
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-630-645-1

  Query Match             100.0%;  Score 40;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8


RESULT 2
US-08-766-596A-1
; Sequence 1, Application US/08766596A
; Patent No. 6462171
;  GENERAL INFORMATION:
;     APPLICANT:  SOTO-JARA, Claudio
;     APPLICANT:  BAUMANN, Marc
;     APPLICANT:  FRANGIONE, Blas
;     TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL
;     TITLE OF INVENTION:  COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;     TITLE OF INVENTION:  ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;     TITLE OF INVENTION:  DEPOSITS
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
```

; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 100.0%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 3
PCT-US96-10220-1
; Sequence 1, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-1

Query Match 100.0%; Score 40; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 4
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES

```
;    TITLE OF INVENTION:  ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;    TITLE OF INVENTION:  DEPOSITS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 400
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,596A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,645
;      FILING DATE:  10-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/478,326
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-766-596A-64

  Query Match              100.0%;  Score 40;  DB 4;  Length 9;
  Best Local Similarity    100.0%;  Pred. No. 3e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 5
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
;  GENERAL INFORMATION:
;    APPLICANT:  Kiessling, Laura L.
```

```
;     APPLICANT:  Murphy, Regina M.
;     TITLE OF INVENTION:  INHIBITORS OF BETA-AMYLOID TOXICITY
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Quarles & Brady
;       STREET:  411 East Wisconsin Avenue
;       CITY:  Milwaukee
;       STATE:  Wisconsin
;       COUNTRY:  U.S.A.
;       ZIP:  53202-4497
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/970,833
;       FILING DATE:
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Baker, Jean C.
;       REGISTRATION NUMBER:  35,433
;       REFERENCE/DOCKET NUMBER:  960296.94291
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (414) 277-5709
;       TELEFAX:  (414) 271-3552
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-970-833-3

  Query Match             100.0%;  Score 40;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.015;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8


RESULT 6
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
;  GENERAL INFORMATION:
;     APPLICANT:  SOTO-JARA, Claudio
;     APPLICANT:  BAUMANN, Marc
;     APPLICANT:  FRANGIONE, Blas
;     TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;     TITLE OF INVENTION:  THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;     TITLE OF INVENTION:  WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
```

```
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 400
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/630,645
;       FILING DATE:
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-630-645-14

  Query Match             100.0%;  Score 40;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 7
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
;  GENERAL INFORMATION:
;     APPLICANT:  SOTO-JARA, Claudio
;     APPLICANT:  BAUMANN, Marc
;     APPLICANT:  FRANGIONE, Blas
;     TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL
;     TITLE OF INVENTION:  COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
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;    TITLE OF INVENTION:  ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;    TITLE OF INVENTION:  DEPOSITS
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 400
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,596A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/630,645
;      FILING DATE:  10-APR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/478,326
;      FILING DATE:  06-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YUN, Allen C.
;      REGISTRATION NUMBER:  37,971
;      REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-766-596A-14

  Query Match             100.0%;  Score 40;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 8
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
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```
;     TITLE OF INVENTION:  THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED
;     TITLE OF INVENTION:  WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
;     NUMBER OF SEQUENCES:  26
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BROWDY AND NEIMARK
;       STREET:  419 Seventh Street, N.W., Suite 400
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/10220
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,645
;       FILING DATE:  10-APR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BROWDY, Roger L.
;       REGISTRATION NUMBER:  25,618
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1 PCT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
PCT-US96-10220-14

  Query Match           100.0%;  Score 40;  DB 5;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.017;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 9
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
;  APPLICANT: Raso, Victor
```

; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-594-366-5

  Query Match   100.0%; Score 40; DB 4; Length 14;
  Best Local Similarity 100.0%; Pred. No. 0.021;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   4 KLVFFAED 11

RESULT 10
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
;   APPLICANT: Findeis, Mark A. et al.
;   TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;   TITLE OF INVENTION: Aggregation
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 28 State Street, Suite 510
;   CITY: Boston
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02109-1875
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/612,785B
;   FILING DATE: Herewith
;   CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/404,831
;   FILING DATE: 14-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/475,579
;   FILING DATE: 07-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: USSN 08/548,998
;   FILING DATE: 27-OCT-1995

```
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  DeConti, Giulio A.
;       REGISTRATION NUMBER:  31,503
;       REFERENCE/DOCKET NUMBER:  PPI-002CP3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)742-4214
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-612-785B-14

  Query Match             100.0%;  Score 40;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          1 KLVFFAED 8


RESULT 11
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
;  GENERAL INFORMATION:
;    APPLICANT:  Findeis, Mark A. et al.
;    TITLE OF INVENTION:  Ab Peptides that Modulate b-Amyloid
;    TITLE OF INVENTION:  Aggregation
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  28 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/612,785B
;      FILING DATE:  Herewith
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/404,831
;      FILING DATE:  14-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  USSN 08/475,579
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
```

; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 100.0%; Score 40; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 6 KLVFFAED 13

RESULT 12
US-08-617-267C-14
; Sequence 14, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 100.0%; Score 40; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 1 KLVFFAED 8

RESULT 13
US-08-766-596A-56
; Sequence 56, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-56

Query Match 100.0%; Score 40; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 5 KLVFFAED 12

RESULT 14
US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 100.0%; Score 40; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 5 KLVFFAED 12

RESULT 15
US-08-766-596A-58
; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.

```
;       COUNTRY:  USA
;       ZIP:  20004
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/766,596A
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/630,645
;       FILING DATE:  10-APR-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/478,326
;       FILING DATE:  06-JUN-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  YUN, Allen C.
;       REGISTRATION NUMBER:  37,971
;       REFERENCE/DOCKET NUMBER:  SOTO-JARA=1A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-628-5197
;       TELEFAX:  202-737-3528
;   INFORMATION FOR SEQ ID NO:  58:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-766-596A-58

  Query Match             100.0%;  Score 40;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          5 KLVFFAED 12


Search completed: March  4, 2004, 15:42:14
Job time : 0.519149 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:30:05 ; Search time 0.434043 Seconds
(without alignments)
1772.942 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	33	2	S23094	beta-amyloid prote
2	40	100.0	42	2	PN0512	beta-amyloid prote
3	40	100.0	57	2	E60045	Alzheimer's diseas
4	40	100.0	57	2	F60045	Alzheimer's diseas
5	40	100.0	57	2	G60045	Alzheimer's diseas
6	40	100.0	57	2	D60045	Alzheimer's diseas
7	40	100.0	57	2	A60045	Alzheimer's diseas
8	40	100.0	57	2	B60045	Alzheimer's diseas
9	40	100.0	82	2	PQ0438	Alzheimer's diseas
10	40	100.0	695	1	A49795	Alzheimer's diseas
11	40	100.0	695	2	A27485	Alzheimer's diseas
12	40	100.0	695	2	S00550	Alzheimer's diseas
13	40	100.0	770	1	QRHUA4	Alzheimer's diseas

14	36	90.0	747	2	JH0773	Alzheimer's diseas
15	34	85.0	321	2	H71729	hypothetical prote
16	32	80.0	182	2	T35807	hypothetical prote
17	32	80.0	261	2	B89868	conserved hypothet
18	31	77.5	119	2	D69345	LSU ribosomal prot
19	31	77.5	641	2	H69651	lichenan operon tr
20	31	77.5	1339	2	T38991	conserved hypothet
21	31	77.5	1364	2	T51920	probable xanthine
22	30	75.0	222	2	T24151	hypothetical prote
23	30	75.0	258	2	AG0459	Sec-independent pr
24	30	75.0	341	2	A64383	hypothetical prote
25	30	75.0	370	2	T47131	G-protein coupled
26	30	75.0	502	2	T27908	hypothetical prote
27	30	75.0	533	2	T46975	lysine-tRNA ligase
28	30	75.0	681	2	T39814	hypothetical prote
29	30	75.0	740	2	S61568	probable membrane
30	30	75.0	768	2	T45876	hypothetical prote
31	30	75.0	1353	2	JC4279	adenylate cyclase
32	29	72.5	99	2	F95064	ribosomal protein
33	29	72.5	99	2	H97931	conserved hypothet
34	29	72.5	100	2	AH1192	B. subtilis YneR p
35	29	72.5	116	1	R5HSS6	ribosomal protein
36	29	72.5	152	2	T06645	hypothetical prote
37	29	72.5	162	2	T13487	NADH2 dehydrogenas
38	29	72.5	162	2	T13563	NADH2 dehydrogenas
39	29	72.5	162	2	T13656	NADH2 dehydrogenas
40	29	72.5	162	2	T13659	NADH2 dehydrogenas
41	29	72.5	164	2	T13562	NADH2 dehydrogenas
42	29	72.5	189	2	S39864	late competence op
43	29	72.5	231	2	H85138	hypothetical prote
44	29	72.5	247	2	B86301	hypothetical prote
45	29	72.5	258	1	S39747	ywfN protein - Bac

ALIGNMENTS

RESULT 1
S23094
beta-amyloid protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase.
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology

Query Match 100.0%; Score 40; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28
```

RESULT 2
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragment for NK-1 substance p receptors.
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid

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  Query Match             100.0%;  Score 40;  DB 2;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         16 KLVFFAED 23
```

RESULT 3
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

```
  Query Match             100.0%;  Score 40;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.078;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28
```

RESULT 4
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: F60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

```
  Query Match             100.0%;  Score 40;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.078;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28
```

RESULT 5
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

```
  Query Match             100.0%;  Score 40;  DB 2;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.078;
```

  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   21 KLVFFAED 28

RESULT 6
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match   100.0%; Score 40; DB 2; Length 57;
  Best Local Similarity   100.0%; Pred. No. 0.078;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   21 KLVFFAED 28

RESULT 7
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide
in dog, polar bear and five other mammals by cross-species polymerase chain
reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: A60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match   100.0%; Score 40; DB 2; Length 57;

  Best Local Similarity   100.0%; Pred. No. 0.078;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   21 KLVFFAED 28

RESULT 8
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C;Species: Ursus maritimus (polar bear)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: B60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: B60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

  Query Match   100.0%; Score 40; DB 2; Length 57;
  Best Local Similarity   100.0%; Pred. No. 0.078;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   21 KLVFFAED 28

RESULT 9
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C;Accession: PQ0438; C60045
R;Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A;Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor protein gene.
A;Reference number: PQ0438; MUID:93075180; PMID:1445331
A;Accession: PQ0438
A;Molecule type: DNA
A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.

A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: C60045
A;Molecule type: mRNA
A;Residues: 12-68 <JOH>
A;Cross-references: EMBL:X56129
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

  Query Match   100.0%; Score 40; DB 2; Length 82;
  Best Local Similarity   100.0%; Pred. No. 0.11;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 KLVFFAED 8
              ||||||||
Db         32 KLVFFAED 39
```

RESULT 10
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlisny, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a primate model for beta amyloidosis in Alzheimer's disease.
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing

  Query Match   100.0%; Score 40; DB 1; Length 695;
  Best Local Similarity   100.0%; Pred. No. 1;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 KLVFFAED 8
              ||||||||
Db        612 KLVFFAED 619
```

RESULT 11
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C;Accession: A27485; S19727; I49485
R;Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987

A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor.
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer related to its human homolog than previously reported.
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>
A;Cross-references: EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer's disease amyloid precursor-encoding gene in mouse.
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; transmembrane protein

  Query Match   100.0%; Score 40; DB 2; Length 695;
  Best Local Similarity   100.0%; Pred. No. 1;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   612 KLVFFAED 619

RESULT 12
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550

A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

  Query Match   100.0%; Score 40; DB 2; Length 695;
  Best Local Similarity   100.0%; Pred. No. 1;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   612 KLVFFAED 619

RESULT 13
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
N;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIa inhibitor; proteinase nexin II (PN-II)
N;Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular form; amyloid protein precursor splice form APP(695); amyloid protein precursor splice form APP(751); amyloid protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44017; B44017; A03134; A29030; A47584; A47585; S02638; S00707; S00925; A38949; A30320; B30320; C30320; A31087; A24668; A28583; A29302; A60805; JL0038;

S06121; A60355; A59011; A38384; S29076; S38252; S32539; S48148; S48692; S51186; S51185; S51184; S51183; A54238; I58075; I52250; S09010; S10737; S24127; S43644
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Beyreuther, K.; Mueller-Hill, B.
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons.
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288,'V',365-770 <LEM1>
A;Cross-references: EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>
A;Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA31830.1; PID:g871360
A;Note: alternative splice form APP(695)
R;La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-protein precursor gene.
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to soybean trypsin inhibitor.
A;Reference number: A33260; MUID:89392030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of hereditary cerebral hemorrhage, Dutch type: DNA and protein diagnostic assays.
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452

A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530,'QWLMPVIPAFWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen, S.G.; Bots, G.T.; Luyendijk, W.; Frangione, B.
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage, Dutch type.
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease.
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-716,'F',718-737 <MUR>
A;Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, L.; O'dahl, S.; Nemens, E.; White, J.A.; Sadovnick, A.D.; Ball, M.J.; Kaye, J.; Warren, A.; McInnis, M.; Antonarakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin, G.M.; Bird, T.D.; Schellenberg, G.D.
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the APP gene region.
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692,'G',694-718 <KAM1>
A;Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380

A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.; Multhaup, G.; Beyreuther, K.; Muller-Hill, B.
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor.
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288,'V',365-770 <KAN>
A;Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular and the neuritic plaque amyloid peptides.
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-646,'E',648-770 <ROB>
A;Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease.
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756,'S',758-770 <GOL>
A;Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Keuren, M.L.; Patterson, D.; Pagan, S.; Kurnit, D.M.; Neve, R.L.
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the Alzheimer locus.
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller-Hill, B.; Masters, C.L.; Beyreuther, K.
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precursor of Alzheimer's disease.
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve, R.L.
Nature 331, 528-530, 1988

A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associated with Alzheimer's disease.
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344,'I',365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Davis, K.; Wallace, W.; Lieberburg, I.; Fuller, F.; Cordell, B.
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors.
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344,'I',365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory activity.
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton, R.A.; Macq, A.F.; Maloteaux, J.M.; Blume, A.J.; Octave, J.N.
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three patients with sporadic Alzheimer's disease.
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288,'V',365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288,'V',365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease brain: coding and noncoding regions of the fetal precursor mRNA are expressed in the cortex.
A;Reference number: A31087; MUID:88124954; PMID:2893379

A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603 as Val, GTG for residue 604 as Glu, GAG for residue 605 as Leu, CTT for residue 607 as Pro, CCC for residue 608 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 655 as Ser
A;Note: the cited Genbank accession number, J03594, is not in release 101.0
R;Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 40; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental regulation of its gene expression.
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

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Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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hypothetical protein RP189 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: H71729

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U.C.M.; Podowski, R.M.; Naeslund, A.K.; Eriksson, A.S.; Winkler, H.H.; Kurland, C.G.
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71729
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-321 <AND>
A;Cross-references: GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA14655.1; PID:e1342498; PID:g3860754; GSPDB:GN00081
A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: RP189
C;Superfamily: Rickettsia prowazekii hypothetical protein RP189

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Job time : 1.43404 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:39:01 ; Search time 0.893617 Seconds
(without alignments)
1890.324 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	40	100.0	8	14	US-10-235-483-1	Sequence 1, Appli
2	40	100.0	9	9	US-09-899-815-2	Sequence 2, Appli
3	40	100.0	9	14	US-10-235-483-64	Sequence 64, Appl
4	40	100.0	11	9	US-09-988-842-9	Sequence 9, Appli
5	40	100.0	11	9	US-09-988-842-25	Sequence 25, Appl
6	40	100.0	11	14	US-10-235-483-14	Sequence 14, Appl
7	40	100.0	13	14	US-10-281-458-1	Sequence 1, Appli
8	40	100.0	14	9	US-09-992-800-5	Sequence 5, Appli
9	40	100.0	14	9	US-09-992-994-5	Sequence 5, Appli
10	40	100.0	14	15	US-10-385-065-5	Sequence 5, Appli
11	40	100.0	15	9	US-09-972-475-14	Sequence 14, Appl
12	40	100.0	15	9	US-09-996-357-9	Sequence 9, Appli
13	40	100.0	15	14	US-10-235-483-56	Sequence 56, Appl
14	40	100.0	15	14	US-10-235-483-57	Sequence 57, Appl
15	40	100.0	15	14	US-10-235-483-58	Sequence 58, Appl
16	40	100.0	15	14	US-10-235-483-63	Sequence 63, Appl
17	40	100.0	15	14	US-10-235-483-65	Sequence 65, Appl
18	40	100.0	15	15	US-10-463-729-14	Sequence 14, Appl
19	40	100.0	17	9	US-09-992-800-3	Sequence 3, Appli
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21	40	100.0	17	10	US-09-998-491-8	Sequence 8, Appli
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23	40	100.0	19	10	US-09-825-242-5	Sequence 5, Appli
24	40	100.0	26	10	US-09-792-079-11	Sequence 11, Appl
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26	40	100.0	28	9	US-09-867-847-4	Sequence 4, Appli
27	40	100.0	28	10	US-09-865-294-66	Sequence 66, Appl
28	40	100.0	28	10	US-09-792-079-5	Sequence 5, Appli
29	40	100.0	28	14	US-10-159-279-5	Sequence 5, Appli
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31	40	100.0	30	14	US-10-301-488A-1	Sequence 1, Appli
32	40	100.0	33	10	US-09-930-915A-295	Sequence 295, App
33	40	100.0	33	14	US-10-082-014-84	Sequence 84, Appl
34	40	100.0	33	14	US-10-372-076-85	Sequence 85, Appl
35	40	100.0	35	9	US-09-867-847-3	Sequence 3, Appli
36	40	100.0	35	9	US-09-972-475-16	Sequence 16, Appl
37	40	100.0	35	15	US-10-463-729-16	Sequence 16, Appl
38	40	100.0	36	9	US-09-861-847-6	Sequence 6, Appli
39	40	100.0	36	9	US-09-861-847-11	Sequence 11, Appl
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41	40	100.0	36	14	US-10-301-488A-11	Sequence 11, Appl
42	40	100.0	39	13	US-10-051-496-5	Sequence 5, Appli
43	40	100.0	39	14	US-10-190-548A-5	Sequence 5, Appli
44	40	100.0	40	9	US-09-861-847-7	Sequence 7, Appli
45	40	100.0	40	9	US-09-861-847-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-235-483-1
; Sequence 1, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio

; BAUMANN, Marc
; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-235-483-1

Query Match 100.0%; Score 40; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KLVFFAED 8

RESULT 2
US-09-899-815-2
; Sequence 2, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT=1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide (16-24 of SEQ ID NO:1)
US-09-899-815-2

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  Best Local Similarity   100.0%; Pred. No. 7.1e+05;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
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Db   1 KLVFFAED 8

RESULT 3
US-10-235-483-64
; Sequence 64, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;   APPLICANT: SOTO-JARA, Claudio
;   BAUMANN, Marc
;   FRANGIONE, Blas
;   TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;   COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;   ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;   DEPOSITS
;   NUMBER OF SEQUENCES: 69
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: BROWDY AND NEIMARK
;   STREET: 419 Seventh Street, N.W., Suite 400
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: USA
;   ZIP: 20004
;   COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-235-483-64

Query Match 100.0%; Score 40; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 2 KLVFFAED 9

RESULT 4
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

  Query Match             100.0%;  Score 40;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9
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RESULT 5
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
;  APPLICANT: Johansson, Jan
;  TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;  TITLE OF INVENTION:  OF AMYLOID FORMATION
;  FILE REFERENCE: 12125-002001
;  CURRENT APPLICATION NUMBER: US/09/988,842
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: US 60/251,662
;  PRIOR FILING DATE: 2000-12-06
;  PRIOR APPLICATION NUMBER: US 60/253,695
;  PRIOR FILING DATE: 2000-11-20
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

  Query Match             100.0%;  Score 40;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9


RESULT 6
US-10-235-483-14
; Sequence 14, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
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;         APPLICANT: SOTO-JARA, Claudio
;                    BAUMANN, Marc
;                    FRANGIONE, Blas
;         TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;                             COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;                             ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;                             DEPOSITS
;         NUMBER OF SEQUENCES: 69
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: BROWDY AND NEIMARK
;              STREET: 419 Seventh Street, N.W., Suite 400
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20004
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/235,483
;              FILING DATE: 06-Sep-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/766,596
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: US 08/630,645
;              FILING DATE: 10-APR-1996
;              APPLICATION NUMBER: US 08/478,326
;              FILING DATE: 06-JUN-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: YUN, Allen C.
;              REGISTRATION NUMBER: 37,971
;              REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 202-628-5197
;              TELEFAX: 202-737-3528
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 11 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: peptide
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-235-483-14

  Query Match             100.0%;  Score 40;  DB 14;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.059;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          2 KLVFFAED 9
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RESULT 7
US-10-281-458-1
; Sequence 1, Application US/10281458
; Publication No. US20030108978A1
; GENERAL INFORMATION:
; APPLICANT: Ciambrone, Gary J.
; APPLICANT: Gibbons, Ian
; TITLE OF INVENTION: Whole Cell Assay Systems for Cell
; TITLE OF INVENTION: Surface Proteases
; FILE REFERENCE: 50225-8093.US03
; CURRENT APPLICATION NUMBER: US/10/281,458
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/337,641
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/924,692
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-281-458-1

  Query Match   100.0%; Score 40; DB 14; Length 13;
  Best Local Similarity   100.0%; Pred. No. 0.071;
  Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 KLVFFAED 8
              ||||||||
Db   6 KLVFFAED 13

RESULT 8
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. US20020102261A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 100.0%; Score 40; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          4 KLVFFAED 11
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RESULT 9
US-09-992-994-5
; Sequence 5, Application US/09992994
; Patent No. US20020136718A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2005
; CURRENT APPLICATION NUMBER: US/09/992,994
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-994-5

Query Match 100.0%; Score 40; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db          4 KLVFFAED 11
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RESULT 10
US-10-385-065-5
; Sequence 5, Application US/10385065
; Publication No. US20030235897A1
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/10/385,065
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US/09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5

; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-385-065-5

  Query Match 100.0%; Score 40; DB 15; Length 14;
  Best Local Similarity 100.0%; Pred. No. 0.077;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
      ||||||||
Db 4 KLVFFAED 11

RESULT 11
US-09-972-475-14
; Sequence 14, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-972-475-14

  Query Match 100.0%; Score 40; DB 9; Length 15;
  Best Local Similarity 100.0%; Pred. No. 0.082;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
  ||||||||
Db 1 KLVFFAED 8

RESULT 12
US-09-996-357-9
; Sequence 9, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Gefter, Malcolm L
; APPLICANT: Isreal, David I
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; TITLE OF INVENTION: TREATING AN AMYLOIDOGENIC DISEASE
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-9

  Query Match 100.0%; Score 40; DB 9; Length 15;
  Best Local Similarity 100.0%; Pred. No. 0.082;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
  ||||||||
Db 1 KLVFFAED 8

RESULT 13
US-10-235-483-56
; Sequence 56, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc

; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-235-483-56

Query Match 100.0%; Score 40; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
||||||||
Db 5 KLVFFAED 12

RESULT 14
US-10-235-483-57
; Sequence 57, Application US/10235483
; Publication No. US20030087407A1
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; BAUMANN, Marc
; FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,483
; FILING DATE: 06-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-235-483-57

Query Match 100.0%; Score 40; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.082;

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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db          5 KLVFFAED 12


RESULT 15
US-10-235-483-58
; Sequence 58, Application US/10235483
; Publication No. US20030087407A1
;   GENERAL INFORMATION:
;        APPLICANT: SOTO-JARA, Claudio
;                   BAUMANN, Marc
;                   FRANGIONE, Blas
;        TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
;                            COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR
DISEASES
;                            ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR
AMYLOID-LIKE
;                            DEPOSITS
;        NUMBER OF SEQUENCES: 69
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 400
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/235,483
;             FILING DATE: 06-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/766,596
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US 08/630,645
;             FILING DATE: 10-APR-1996
;             APPLICATION NUMBER: US 08/478,326
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: YUN, Allen C.
;             REGISTRATION NUMBER: 37,971
;             REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-235-483-58

  Query Match 100.0%; Score 40; DB 14; Length 15;
  Best Local Similarity 100.0%; Pred. No. 0.082;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8
  ||||||||
Db 5 KLVFFAED 12

Search completed: March 4, 2004, 15:57:37
Job time : 0.893617 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:28:35 ; Search time 1.14894 Seconds
(without alignments)
2196.942 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description

1	40	100.0	28	4	Q9UCD1	Q9ucd1 homo sapien
2	40	100.0	30	4	Q9UCA9	Q9uca9 homo sapien
3	40	100.0	33	4	Q9UC33	Q9uc33 homo sapien
4	40	100.0	79	11	O35463	O35463 cricetulus
5	40	100.0	82	4	Q16020	Q16020 homo sapien
6	40	100.0	82	4	Q16014	Q16014 homo sapien
7	40	100.0	82	4	Q16019	Q16019 homo sapien
8	40	100.0	113	13	Q8JH58	Q8jh58 chelydra se
9	40	100.0	218	11	Q8BPV5	Q8bpv5 mus musculu
10	40	100.0	357	13	Q8UUI8	Q8uui8 brachydanio
11	40	100.0	384	11	Q8BPC7	Q8bpc7 mus musculu
12	40	100.0	472	13	Q8UUS0	Q8uus0 brachydanio
13	40	100.0	534	13	O93296	O93296 gallus gall
14	40	100.0	569	13	Q9PVL1	Q9pvl1 gallus gall
15	40	100.0	612	13	Q9I9E7	Q9i9e7 brachydanio
16	40	100.0	678	13	Q7ZZT1	Q7zzt1 brachydanio
17	40	100.0	695	13	Q9DGJ8	Q9dgj8 gallus gall
18	40	100.0	738	13	Q90W28	Q90w28 brachydanio
19	40	100.0	751	13	Q9DGJ7	Q9dgj7 gallus gall
20	37	92.5	1676	16	Q8A6R7	Q8a6r7 bacteroides
21	36	90.0	693	13	Q98SG0	Q98sg0 xenopus lae
22	36	90.0	747	13	Q91963	Q91963 xenopus. ap
23	33	82.5	162	8	Q32406	Q32406 heteranther
24	33	82.5	197	16	Q7VR77	Q7vr77 candidatus
25	33	82.5	695	13	Q98SF9	Q98sf9 xenopus lae
26	33	82.5	695	13	Q7ZXQ0	Q7zxq0 xenopus lae
27	32	80.0	182	16	Q9Z588	Q9z588 streptomyce
28	32	80.0	184	16	Q931V3	Q931v3 staphylococ
29	32	80.0	261	2	Q7X225	Q7x225 staphylococ
30	32	80.0	261	2	Q7WRM0	Q7wrm0 staphylococ
31	32	80.0	261	16	Q99V89	Q99v89 staphylococ
32	32	80.0	268	16	Q8NXD0	Q8nxd0 staphylococ
33	32	80.0	282	16	Q8CUH9	Q8cuh9 oceanobacil
34	32	80.0	472	13	Q10833	Q10833 xenopus lae
35	32	80.0	501	16	Q7UZT9	Q7uzt9 prochloroco
36	32	80.0	1105	5	Q9VX31	Q9vx31 drosophila
37	32	80.0	2613	5	Q9GYD1	Q9gyd1 leishmania
38	31	77.5	49	6	O97917	O97917 bos taurus
39	31	77.5	147	16	Q8A5K5	Q8a5k5 bacteroides
40	31	77.5	179	16	Q82JK4	Q82jk4 streptomyce
41	31	77.5	208	16	Q8ESR7	Q8esr7 oceanobacil
42	31	77.5	228	16	Q8E2V5	Q8e2v5 streptococc
43	31	77.5	228	16	Q8DX05	Q8dx05 streptococc
44	31	77.5	248	5	Q8I3W8	Q8i3w8 plasmodium
45	31	77.5	259	16	Q8NN32	Q8nn32 corynebacte

ALIGNMENTS

RESULT 1
Q9UCD1
ID   Q9UCD1   PRELIMINARY;   PRT;   28 AA.
AC   Q9UCD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94045685; PubMed=8229004;
RA   Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;
RT   "Characterization of beta-amyloid peptide from human cerebrospinal
RT   fluid.";
RL   J. Neurochem. 61:1965-1968(1993).
DR   HSSP; P05067; 1AMB.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   28 AA;  3244 MW;  DE7BD081160AFC81 CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         16 KLVFFAED 23


RESULT 2
Q9UCA9
ID   Q9UCA9      PRELIMINARY;      PRT;    30 AA.
AC   Q9UCA9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=94153015; PubMed=8109908;
RA   Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT   "The amino acid sequence of neuritic plaque amyloid from a familial
RT   Alzheimer's disease patient.";
RL   Ann. Neurol. 35:245-246(1994).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   30 AA;  3391 MW;  FF4167ABD081160A CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.23;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
```

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                ||||||||
Db          16 KLVFFAED 23


RESULT 3
Q9UC33
ID   Q9UC33      PRELIMINARY;      PRT;    33 AA.
AC   Q9UC33;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=93024877; PubMed=1406936;
RA   Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA   Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT   "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT   biological fluids.";
RL   Nature 359:325-327(1992).
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
SQ   SEQUENCE   33 AA;  3674 MW;  B1DEFE2F4167ABD0 CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 0.25;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 KLVFFAED 8
                ||||||||
Db          16 KLVFFAED 23


RESULT 4
O35463
ID   O35463      PRELIMINARY;      PRT;    79 AA.
AC   O35463;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alzheimer's amyloid beta protein (Fragment).
GN   BETA APP.
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sambamurti K., Pinnix I., Gandhi S.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
```

```
DR   EMBL; AF030413; AAB86608.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      79     79
SQ   SEQUENCE   79 AA;  8538 MW;  37F2C6C3BFF3F597 CRC64;

  Query Match             100.0%;  Score 40;  DB 11;  Length 79;
  Best Local Similarity   100.0%;  Pred. No. 0.58;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         36 KLVFFAED 43
```

```
RESULT 5
Q16020
ID   Q16020      PRELIMINARY;      PRT;    82 AA.
AC   Q16020;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61383; AAB26265.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8882 MW;  F534AA5AE5D9230A CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         33 KLVFFAED 40


RESULT 6
```

```
Q16014
ID   Q16014      PRELIMINARY;      PRT;    82 AA.
AC   Q16014;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S60721; AAB26263.2; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8972 MW;  F534AA5B3EA9230A CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         33 KLVFFAED 40


RESULT 7
Q16019
ID   Q16019      PRELIMINARY;      PRT;    82 AA.
AC   Q16019;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-amyloid peptide (Fragment).
GN   BETA APP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93236601; PubMed=8476439;
RA   Denman R.B., Rosenzcwaig R., Miller D.L.;
RT   "A system for studying the effect(s) of familial Alzheimer disease
RT   mutations on the processing of the beta-amyloid peptide precursor.";
RL   Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR   EMBL; S61380; AAB26264.2; -.
```

```
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
FT   NON_TER       1      1
FT   NON_TER      82     82
SQ   SEQUENCE   82 AA;  8938 MW;  F534AA50E579230A CRC64;

  Query Match             100.0%;  Score 40;  DB 4;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 0.61;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         33 KLVFFAED 40


RESULT 8
Q8JH58
ID   Q8JH58      PRELIMINARY;      PRT;   113 AA.
AC   Q8JH58;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid beta protein (Fragment).
OS   Chelydra serpentina serpentina (common snapping turtle).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
OX   NCBI_TaxID=134619;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21876906; PubMed=11882478;
RA   Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT   "Octylphenol (OP) alters the expression of members of the amyloid
RT   protein family in the hypothalamus of the snapping turtle, Chelydra
RT   serpentina serpentina.";
RL   Environ. Health Perspect. 110:269-275(2002).
DR   EMBL; AF541917; AAN04908.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   113 AA;  12750 MW;  72515C930496E053 CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 0.83;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         30 KLVFFAED 37


RESULT 9
```

```
Q8BPV5
ID   Q8BPV5      PRELIMINARY;      PRT;   218 AA.
AC   Q8BPV5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Lung;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK052448; BAC34997.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   218 AA;  24118 MW;  95B55AFDAE1D0EF5 CRC64;

  Query Match             100.0%;  Score 40;  DB 11;  Length 218;
  Best Local Similarity   100.0%;  Pred. No. 1.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        135 KLVFFAED 142


RESULT 10
Q8UUI8
ID   Q8UUI8      PRELIMINARY;      PRT;   357 AA.
AC   Q8UUI8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative mebrane protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Embryo;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315637; CAC85734.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   357 AA;  40962 MW;  07D99EEF6C55B2D8 CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 357;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        274 KLVFFAED 281


RESULT 11
Q8BPC7
ID   Q8BPC7      PRELIMINARY;      PRT;   384 AA.
AC   Q8BPC7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid beta (Fragment).
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK076506; BAC36369.1; -.
DR   MGD; MGI:88059; App.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
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```
SQ   SEQUENCE   384 AA;  43990 MW;  A81B1AD8AE683173 CRC64;

  Query Match             100.0%;  Score 40;  DB 11;  Length 384;
  Best Local Similarity   100.0%;  Pred. No. 2.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        301 KLVFFAED 308


RESULT 12
Q8UUS0
ID   Q8UUS0      PRELIMINARY;      PRT;   472 AA.
AC   Q8UUS0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative membrane protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   PubMed=11862463;
RA   Musa A., Lehrach H., Russo V.E.A.;
RT   "Distinct expression patterns of two zebrafish homologues of the human
RT   APP gene during embryonic development.";
RL   Dev. Genes Evol. 211:563-567(2001).
DR   EMBL; AJ315636; CAC85733.1; -.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   472 AA;  53787 MW;  24F7128BE3356550 CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 472;
  Best Local Similarity   100.0%;  Pred. No. 3.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        389 KLVFFAED 396


RESULT 13
O93296
ID   O93296      PRELIMINARY;      PRT;   534 AA.
AC   O93296;
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DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98337885; PubMed=9671674;
RA   Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA   Milligan C.E.;
RT   "Increased production of amyloid precursor protein provides a
RT   substrate for caspase-3 in dying motoneurons.";
RL   J. Neurosci. 18:5869-5880(1998).
DR   EMBL; AF042098; AAC25052.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   534 AA;  60597 MW;  FB53ECC2E66D4C92 CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 534;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        451 KLVFFAED 458


RESULT 14
Q9PVL1
ID   Q9PVL1      PRELIMINARY;      PRT;   569 AA.
AC   Q9PVL1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
```

```
RA   Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT   "What the evolution of the amyloid protein precursor supergene family
RT   tells us about its function.";
RL   Neurochem. Int. 0:0-0(2000).
DR   EMBL; AF030341; AAF12698.1; -.
DR   HSSP; P05067; 1BA4.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   569 AA;  64753 MW;  0AB8BB851863A19D CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        487 KLVFFAED 494


RESULT 15
Q9I9E7
ID   Q9I9E7      PRELIMINARY;      PRT;   612 AA.
AC   Q9I9E7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Amyloid protein (Fragment).
GN   APPA.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Slavov D.B., Gardiner K.;
RT   "An App cDNA from Zebrafish (Danio rerio).";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF257742; AAF71748.1; -.
DR   HSSP; P05067; 1HZ3.
DR   ZFIN; ZDB-GENE-000616-13; appa.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PROSITE; PS00319; A4_EXTRA; 1.
```

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DR   PROSITE; PS00320; A4_INTRA; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   612 AA;  69710 MW;  59A9ACBDF9C59EFF CRC64;

  Query Match             100.0%;  Score 40;  DB 13;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        529 KLVFFAED 536


Search completed: March  4, 2004, 15:38:54
Job time : 2.14894 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 15:22:30 ; Search time 0.255319 Seconds
(without alignments)
1631.532 Million cell updates/sec

Title: US-09-668-314C-73
Perfect score: 40
Sequence: 1 KLVFFAED 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	57	1	A4_URSMA	Q29149 ursus marit
2	40	100.0	58	1	A4_CANFA	Q28280 canis famil
3	40	100.0	58	1	A4_RABIT	Q28748 oryctolagus
4	40	100.0	58	1	A4_SHEEP	Q28757 ovis aries
5	40	100.0	59	1	A4_BOVIN	Q28053 bos taurus
6	40	100.0	751	1	A4_SAISC	Q95241 s amyloid b
7	40	100.0	770	1	A4_CAVPO	Q60495 c amyloid b
8	40	100.0	770	1	A4_HUMAN	P05067 h amyloid b
9	40	100.0	770	1	A4_MACFA	P53601 m amyloid b
10	40	100.0	770	1	A4_MOUSE	P12023 m amyloid b
11	40	100.0	770	1	A4_PIG	P79307 s amyloid b
12	40	100.0	770	1	A4_RAT	P08592 r amyloid b
13	40	100.0	780	1	A4_TETFL	O73683 tetraodon f
14	37	92.5	737	1	A4_FUGRU	O93279 fugu rubrip
15	34	85.0	321	1	Y189_RICPR	Q9zdx5 rickettsia
16	31	77.5	119	1	RL7A_ARCFU	O29494 archaeoglob
17	31	77.5	281	1	UPK_CORST	Q9fb58 corynebacte
18	31	77.5	641	1	LICR_BACSU	P46321 bacillus su

19	31	77.5	2196	1	MOR2_SCHPO	Q9hdv6 schizosacch
20	30	75.0	214	1	UT11_ORYSA	Q8s1z1 oryza sativ
21	30	75.0	341	1	Y665_METJA	Q58079 methanococc
22	30	75.0	370	1	GP85_HUMAN	Q9npd1 homo sapien
23	30	75.0	371	1	GP85_BRARE	Q9i919 brachydanio
24	30	75.0	533	1	SYK_METMP	O30522 methanococc
25	30	75.0	1353	1	CYA9_HUMAN	O60503 homo sapien
26	30	75.0	1353	1	CYA9_MOUSE	P51830 mus musculu
27	29	72.5	119	1	RL7A_HALMA	P12743 haloarcula
28	29	72.5	189	1	CME2_BACSU	P32393 bacillus su
29	29	72.5	258	1	RSFA_BACSU	P39650 bacillus su
30	29	72.5	278	1	ERA_BUCAP	Q8k9r2 buchnera ap
31	29	72.5	286	1	DMA_HAEIN	P44431 haemophilus
32	29	72.5	357	1	HST2_YEAST	P53686 saccharomyc
33	29	72.5	469	1	RECJ_METJA	Q58387 methanococc
34	29	72.5	481	1	RNF9_PANTR	Q7yr32 pan troglod
35	29	72.5	482	1	RNF9_HUMAN	Q9udy6 homo sapien
36	29	72.5	634	1	ELM1_ASPFU	P46074 aspergillus
37	29	72.5	634	1	ELM2_ASPFU	P46075 aspergillus
38	29	72.5	809	1	KCB2_CANFA	Q95167 canis famil
39	29	72.5	857	1	KCB1_MOUSE	Q03717 mus musculu
40	29	72.5	857	1	KCB1_RAT	P15387 rattus norv
41	29	72.5	858	1	KCB1_HUMAN	Q14721 homo sapien
42	29	72.5	858	1	KCB1_PIG	O18868 sus scrofa
43	29	72.5	858	1	KCB1_RABIT	Q9mz19 oryctolagus
44	29	72.5	907	1	KCB2_RAT	Q63099 rattus norv
45	29	72.5	911	1	KCB2_HUMAN	Q92953 homo sapien

ALIGNMENTS

```
RESULT 1
A4_URSMA
ID   A4_URSMA       STANDARD;      PRT;    57 AA.
AC   Q29149;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ursus maritimus (Polar bear) (Thalarctos maritimus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX   NCBI_TaxID=29073;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
```

```
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56128; CAA39593.1; -.
DR   PIR; B60045; B60045.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   NON_TER      57     57
SQ   SEQUENCE   57 AA;  6172 MW;  84209D88EBA82DFA CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 2
A4_CANFA
ID   A4_CANFA       STANDARD;      PRT;    58 AA.
AC   Q28280;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
```

```
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56125; CAA39590.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6285 MW;  8469D488A2E12DFA CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         22 KLVFFAED 29


RESULT 3
A4_RABIT
ID   A4_RABIT       STANDARD;      PRT;    58 AA.
AC   Q28748;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56129; CAA39594.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 4
A4_SHEEP
ID   A4_SHEEP        STANDARD;      PRT;    58 AA.
AC   Q28757;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Ovis aries (Sheep).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X56130; CAA39595.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         6     48       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     33       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     34     57       POTENTIAL.
FT   DOMAIN       58    >58       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      58     58
SQ   SEQUENCE   58 AA;  6300 MW;  F434209D88EBA82D CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         21 KLVFFAED 28


RESULT 5
A4_BOVIN
ID   A4_BOVIN        STANDARD;      PRT;    59 AA.
AC   Q28053;
DT   01-NOV-1997 (Rel. 35, Created)
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DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE   protein (Beta-APP) (A-beta)] (Fragment).
GN   APP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56124; CAA39589.1; -.
DR   EMBL; X56126; CAA39591.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR001255; Beta-APP.
DR   Pfam; PF03494; Beta-APP; 1.
DR   PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR   PROSITE; PS00320; A4_INTRA; PARTIAL.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane.
FT   NON_TER       1      1
FT   CHAIN         7     49       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       <1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     58       POTENTIAL.
FT   DOMAIN       59    >59       CYTOPLASMIC (POTENTIAL).
FT   NON_TER      59     59
SQ   SEQUENCE   59 AA;  6414 MW;  F43469D488A2E12D CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db         22 KLVFFAED 29
```

```
RESULT 6
A4_SAISC
ID   A4_SAISC        STANDARD;      PRT;   751 AA.
AC   Q95241;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE   APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE   Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE   CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE   (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE   secretase C-terminal fragment 50); C31].
GN   APP.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Liver;
RX   MEDLINE=96108492; PubMed=8532114;
RA   Levy E., Amorim A., Frangione B., Walker L.C.;
RT   "Beta-amyloid precursor protein gene in squirrel monkeys with
RT   cerebral amyloid angiopathy.";
RL   Neurobiol. Aging 16:805-808(1995).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction. In vitro, copper-metallated APP induces neuronal
CC       death directly or is potentiated through Cu(II)-mediated low-
CC       density lipoprotein oxidation (By similarity). Can regulate
CC       neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
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CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=Q95241-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q95241-2; Sequence=Not described;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
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CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81024; AAD14347.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Amyloid; Alternative splicing.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    751       A4 PROTEIN.
FT   CHAIN        18    668       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    652       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       653    751       C99 (POTENTIAL).
FT   CHAIN       653    694       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
FT   CHAIN       653    692       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN       669    751       C83 (POTENTIAL).
FT   CHAIN       669    694       P3(42) (POTENTIAL).
FT   CHAIN       669    692       P3(40) (POTENTIAL).
FT   CHAIN       693    751       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN       695    751       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN       702    751       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN       721    751       C31 (POTENTIAL).
FT   DOMAIN       18    680       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    681    704       POTENTIAL.
FT   DOMAIN      705    751       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
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FT   DOMAIN       181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       316    344       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       363    428       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       504    521       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       713    732       INTERACTION WITH G(O)-ALPHA
FT                                 (BY SIMILARITY).
FT   DOMAIN       230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274    280       POLY-THR.
FT   SITE         144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                 (BY SIMILARITY).
FT   ACT_SITE     301    302       REACTIVE BOND.
FT   SITE         652    653       CLEAVAGE (BY BETA-SECRETASE)
FT                                 (BY SIMILARITY).
FT   SITE         653    654       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         668    669       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                 (BY SIMILARITY).
FT   SITE         685    685       INVOLVED IN FREE RADICAL PROPAGATION
FT                                 (BY SIMILARITY).
FT   SITE         687    687       INVOLVED IN OXIDATIVE REACTIONS
FT                                 (BY SIMILARITY).
FT   SITE         692    693       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                 (BY SIMILARITY).
FT   SITE         694    695       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                 (BY SIMILARITY).
FT   SITE         701    702       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                 (BY SIMILARITY).
FT   SITE         705    715       BASOLATERAL SORTING SIGNAL
FT                                 (BY SIMILARITY).
FT   SITE         720    721       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)
FT                                 (BY SIMILARITY).
FT   SITE         738    741       ENDOCYTOSIS SIGNAL.
FT   SITE         740    743       NPXY MOTIF.

  Query Match             100.0%;  Score 40;  DB 1;  Length 751;
  Best Local Similarity   100.0%;  Pred. No. 0.37;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy            1 KLVFFAED 8
                |||||||
Db          668 KLVFFAED 675


RESULT 7
A4_CAVPO
ID   A4_CAVPO        STANDARD;      PRT;   770 AA.
AC   Q60495; Q60496;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE   Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
DE   protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
DE   P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
DE   CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
GN   APP.
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OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain, and Liver;
RX   MEDLINE=97236426; PubMed=9116031;
RA   Beck M., Mueller D., Bigl V.;
RT   "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT   alternative splicing.";
RL   Biochim. Biophys. Acta 1351:17-21(1997).
RN   [2]
RP   INTERACTION OF BETA-APP40 WITH APOE.
RX   MEDLINE=98007700; PubMed=9349544;
RA   Martel C.L., Mackic J.B., Matsubara E., Governale S., Miguel C.,
RA   Miao W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
RT   "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
RT   cerebral capillary sequestration and blood-brain barrier transport of
RT   circulating Alzheimer's amyloid beta.";
RL   J. Neurochem. 69:1995-2004(1997).
RN   [3]
RP   PROCESSING.
RX   MEDLINE=20084499; PubMed=10619481;
RA   Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA   Bigl V.;
RT   "Guinea-pig primary cell cultures provide a model to study expression
RT   and amyloidogenic processing of endogenous amyloid precursor
RT   protein.";
RL   Neuroscience 95:243-254(2000).
RN   [4]
RP   GAMMA-SECRETASE PROCESSING.
RX   MEDLINE=20576391; PubMed=11035007;
RA   Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA   Ziani-Cherif C., Onstead L., Sambamurti K.;
RT   "A novel gamma -secretase assay based on detection of the putative
RT   C-terminal fragment-gamma of amyloid beta protein precursor.";
RL   J. Biol. Chem. 276:481-487(2001).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
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CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC       and apoliproteins E and J in the CSF and to HDL particles in
CC       plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC   -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC       extracellular matrix and may regulate neurite outgrowth in the
CC       brain (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains), APPBP2 (via BaSS) and DDB1 (By similarity).
CC       Associates with microtubules in the presence of ATP and in a
CC       kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC       all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC       ApoE3 appears to be the preferred amyloid binding isoform, while
CC       the apoE4 isoform-beta-APP40 complex is capable of being
CC       transported across the blood-brain barrier.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated pits
CC       (By similarity). During maturation, the immature APP (N-
CC       glycosylated in the endoplasmic reticulum) moves to the Golgi
CC       complex where complete maturation occurs (O-glycosylated and
CC       sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC       APP is released into the extracellular space and the C-terminal is
CC       internalized to endosomes and lysosomes (By similarity). Some APP
CC       accumulates in secretory transport vesicles leaving the late Golgi
CC       compartment and returns to the cell surface (By similarity). APP
CC       sorts to the basolateral surface in epithelial cells (By
CC       similatity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms, missing exons 7,8 and 15, seem to
CC         exist. The L-isoforms, missing exon 15, are referred to as
CC         appicans;
CC       Name=APP770;
CC         IsoId=Q60495-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC   -!- TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC       brain. The longer isoforms containing the BPTI domain are
CC       predominantly expressed in peripheral organs such as muscle and
CC       liver.
CC   -!- INDUCTION: Increased levels during neuronal differentiation.
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells.
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
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CC       are independent of phosphorylation on the terminal tyrosine
CC       residue (By similarity). The NPXY site is also involved in
CC       clathrin-mediated endocytosis.
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC       gamma-secretase yields P3 peptides. This is the major secretory
CC       pathway and is nonamyloidogenic. Alternatively,
CC       presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC       beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC       and amyloid-beta 42 (Abeta42), major components of amyloid
CC       plaques, and the corresponding cytotoxic C-terminal fragments
CC       (CTFs).
CC   -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC       apoptosis (By similarity).
CC   -!- PTM: N- and O-glycosylated. O-linkage of chondroitin sulfate to
CC       the L-APP isoforms produces the APP proteoglycan core proteins,
CC       the appicans (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific (By similarity).
CC       Phosphorylation can affect APP processing, neuronal
CC       differentiation and interaction with other proteins.
CC   -!- PTM: Extracellular binding and reduction of copper, results in a
CC       corresponding oxidation of Cys-144 and Cys-158, and the formation
CC       of a disulfide bond (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X97631; CAA66230.1; -.
DR   EMBL; X99198; CAA67589.1; -.
DR   HSSP; P05067; 1BA4.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (BY SIMILARITY).
FT   CHAIN        18    671       SOLUBLE APP-BETA (BY SIMILARITY).
FT   CHAIN       672    770       CTF-ALPHA (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       CTF-BETA (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59) (BY SIMILARITY).
FT   CHAIN       714    770       GAMMA-CTF(57) (BY SIMILARITY).

  Query Match             100.0%;  Score 40;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694


RESULT 8
A4_HUMAN
ID   A4_HUMAN        STANDARD;      PRT;   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q16014;
AC   Q16019; Q16020; Q9BT38; Q9UCA9; Q9UCB6; Q9UCC8; Q9UCD1; Q9UQ58;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
GN   APP OR A4 OR AD1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=87144572; PubMed=2881207;
RA   Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA   Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
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RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [5]
RP ERRATUM, AND REVISIONS.
RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RL Gene 102:291-292(1991).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
RC TISSUE=Leukocyte;
RX MEDLINE=92268136; PubMed=1587857;
RA Koenig G., Moenning U., Czech C., Prior R., Banati R.,
RA Schreiter-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
RT "Identification and differential expression of a novel alternative
RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
RT leukocytes and brain microglial cells.";
RL J. Biol. Chem. 267:10804-10809(1992).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM APP639).
RC TISSUE=Brain;
RX MEDLINE=22744650; PubMed=12859342;
RA Tang K., Wang C., Shen C., Sheng S., Ravid R., Jing N.;
RT "Identification of a novel alternative splicing isoform of human
RT amyloid precursor protein gene, APP639.";
RL Eur. J. Neurosci. 18:102-108(2003).

RN [9]
RP SEQUENCE FROM N.A. (ISOFORM APP305).
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [11]
RP ERRATUM, AND REVISIONS.
RA Mita S., Sadlock J., Herbert J., Schon E.A.;
RL Nucleic Acids Res. 16:11402-11402(1988).
RN [12]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89165870; PubMed=2538123;
RA La Fauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
RT "Characterization of the 5'-end region and the first two exons of the
RT beta-protein precursor gene.";
RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
RN [13]
RP SEQUENCE OF 18-50.
RC TISSUE=Fibroblast;
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [14]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
RC TISSUE=Brain;
RX MEDLINE=89346754; PubMed=2569763;
RA de Sauvage F., Octave J.N.;
RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
RT secreted protein.";

RL Science 245:651-653(1989).
RN [15]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [16]
RP SEQUENCE OF 286-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [17]
RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [18]
RP SEQUENCE OF 507-770 FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [19]
RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
RX MEDLINE=96139497; PubMed=8576160;
RA Beher D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RT mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [20]
RP SEQUENCE OF 655-737 FROM N.A., AND VARIANTS AD PHE-717; AD ILE-717
RP AND AD GLY-717.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzcwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
RN [21]
RP SEQUENCE OF 656-737 FROM N.A.
RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).

RN [22]

Query Match 100.0%; Score 40; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694
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RESULT 9
A4_MACFA
ID A4_MACFA STANDARD; PRT; 770 AA.
AC P53601; Q95KN7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metallated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By

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CC       similarity). The splice isoforms that contain the BPTI domain
CC       possess protease inhibitor activity (By similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
CC       space and the C-terminal is internalized to endosomes and
CC       lysosomes. Some APP accumulates in secretory transport vesicles
CC       leaving the late Golgi compartment and returns to the cell
CC       surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC       and nuclei of neurons (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=APP770;
CC         IsoId=P53601-1; Sequence=Displayed;
CC       Name=APP695;
CC         IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC   -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC       sorting of membrane proteins to the basolateral surface of
CC       epithelial cells (By similarity).
CC   -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC       phosphorylated proteins is required for the specific binding of
CC       the PID domain. However additional amino acids either N- or C-
CC       terminal to the NPXY motif are often required for complete
CC       interaction. The PID domain-containing proteins which bind APP
CC       require the YENPTY motif for full interaction. These interactions
CC       are independent of phosphorylation on the terminal tyrosine
CC       residue. The NPXY site is also involved in clathrin-mediated
CC       endocytosis (By similarity).
CC   -!- PTM: Proteolytically processed under normal cellular conditions.
CC       Cleavage by alpha-secretase or alternatively by beta-secretase
CC       leads to generation and extracellular release of soluble APP
CC       peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC       retention of corresponding membrane-anchored C-terminal fragments,
CC       C83 and C99. Subsequent processing of C83 by gamma-secretase
CC       yields P3 peptides. This is the major secretory pathway and is
CC       nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC       gamma-secretase processing of C99 releases the amyloid beta
CC       proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
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CC       major components of amyloid plaques, and the cytotoxic C-terminal
CC       fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC       similarity).
CC   -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC       (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC       results in the production of the neurotoxic C31 peptide and the
CC       increased production of beta-amyloid peptides (By similarity).
CC   -!- PTM: N- and O-glycosylated (By similarity).
CC   -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC       serine residues is neuron-specific. Phosphorylation can affect APP
CC       processing, neuronal differentiation and interaction with other
CC       proteins (By similarity).
CC   -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC       zinc, can induce histidine-bridging between beta-amyloid molecules
CC       resulting in beta-amyloid-metal aggregates (By similarity).
CC       Extracellular zinc-binding increases binding of heparin to APP and
CC       inhibits collagen-binding (By similarity).
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M58727; AAA36829.1; -.
DR   EMBL; M58726; AAA36828.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Proteoglycan; Alternative splicing; Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (POTENTIAL).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (POTENTIAL).
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FT   CHAIN        672    711       BETA-AMYLOID PROTEIN 40 (POTENTIAL).
FT   CHAIN        688    770       C83 (POTENTIAL).
FT   CHAIN        688    713       P3(42) (POTENTIAL).
FT   CHAIN        688    711       P3(40) (POTENTIAL).
FT   CHAIN        712    770       GAMMA-CTF(59) (POTENTIAL).
FT   CHAIN        714    770       GAMMA-CTF(57) (POTENTIAL).
FT   CHAIN        721    770       GAMMA-CTF(50) (POTENTIAL).
FT   CHAIN        740    770       C31 (POTENTIAL).
FT   DOMAIN        18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     700    723       POTENTIAL.
FT   DOMAIN       724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN       291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN       391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN       523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN       732    751       INTERACTION WITH G(O)-ALPHA
FT                                  (BY SIMILARITY).
FT   DOMAIN       230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN       274    280       POLY-THR.
FT   SITE         144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                  (BY SIMILARITY).
FT   ACT_SITE     301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE         671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE         687    688       CLEAVAGE (BY ALPHA-SECRETASE)
FT                                  (BY SIMILARITY).
FT   SITE         704    704       IMPLICATED IN FREE RADICAL PROPAGATION
FT                                  (BY SIMILARITY).
FT   SITE         706    706       INVOLVED IN OXIDATIVE REACTIONS
FT                                  (BY SIMILARITY).
FT   SITE         711    712       CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                  (BY SIMILARITY).
FT   SITE         713    714       CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                  (BY SIMILARITY).
FT   SITE         720    721       CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT                                  (BY SIMILARITY).
FT   SITE         724    734       BASOLATERAL SORTING SIGNAL
FT                                  (BY SIMILARITY).
FT   SITE         739    740       CLEAVAGE (BY CASPASES-3,-6,-8 OR -9)

  Query Match             100.0%;  Score 40;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694


RESULT 10
A4_MOUSE
ID   A4_MOUSE        STANDARD;      PRT;   770 AA.
AC   P12023; P97487; P97942; Q99K32;
DT   01-OCT-1989 (Rel. 12, Created)
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DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains:
DE   Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99
DE   (APP-C99); Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein
DE   40 (Beta-APP40); C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase
DE   C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE   (APP-C59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)
DE   (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-CTF(50)
DE   (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE   50) (AID(50)); C31].
GN   APP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88106489; PubMed=3322280;
RA   Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT   "Complementary DNA for the mouse homolog of the human amyloid beta
RT   protein precursor.";
RL   Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN   [2]
RP   REVISIONS.
RA   Yamada T.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=BALB/c; TISSUE=Brain;
RX   MEDLINE=92096458; PubMed=1756177;
RA   de Strooper B., van Leuven F., van den Berghe H.;
RT   "The amyloid beta protein precursor or proteinase nexin II from mouse
RT   is closer related to its human homolog than previously reported.";
RL   Biochim. Biophys. Acta 1129:141-143(1991).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   STRAIN=SAMP8; TISSUE=Hippocampus;
RX   MEDLINE=21130647; PubMed=11235921;
RA   Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
RA   Alvarez J., Morley J.E.;
RT   "Molecular cloning, expression, and regulation of hippocampal amyloid
RT   precursor protein of senescence accelerated mouse (SAMP8).";
RL   Biochem. Cell Biol. 79:57-67(2001).
RN   [5]
RP   SEQUENCE OF 1-19 FROM N.A.
RX   MEDLINE=92209998; PubMed=1555768;
RA   Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA   Sakai Y.;
RT   "Positive and negative regulatory elements for the expression of the
RT   Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RL   Gene 112:189-195(1992).
RN   [6]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC   TISSUE=Breast tumor;
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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
RN [8]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RT precursor of Mus domesticus.";
RL Nucleic Acids Res. 17:5396-5396(1989).
RN [9]
RP SEQUENCE OF 656-737 FROM N.A.
RC STRAIN=129/Sv;
RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecchi M.,
RA Loring J.F., Goate A.M.;
RT "Introduction of six mutations into the mouse genome using 'Hit and
RT Run' gene-targeting: introduction of familial Alzheimer's disease
RT mutations into the mouse amyloid precursor protein gene and
RT humanization of the A-beta fragment.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
RX MEDLINE=93287808; PubMed=8510506;
RA Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.;
RT "Regional distribution of the alternatively spliced isoforms of beta
RT APP RNA transcript in the brain of normal, heterozygous and
RT homozygous weaver mutant mice as revealed by in situ hybridization
RT histochemistry.";
RL Brain Res. Mol. Brain Res. 17:340-346(1993).

RN [11]
RP INTERACTION WITH KNS2.
RX MEDLINE=21010507; PubMed=11144355;
RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
RT "Axonal transport of amyloid precursor protein is mediated by direct
RT binding to the kinesin light chain subunit of kinesin-I.";
RL Neuron 28:449-459(2000).
RN [12]
RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-728;
RP THR-743; TYR-757; ASN-759 AND TYR-762.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [13]
RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
RX MEDLINE=22028091; PubMed=11912189;
RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.;
RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
RT with scaffold proteins of the JNK signaling cascade.";
RL J. Biol. Chem. 277:20070-20078(2002).
RN [14]
RP INTERACTION OF CTF PEPTIDES WITH NUMB.
RX MEDLINE=22008109; PubMed=12011466;
RA Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
RA Meucci O., McGlade J.C., Rakic P., D'Adamio L.;
RT "The gamma-secretase-generated intracellular domain of beta-amyloid
RT precursor protein binds Numb and inhibits Notch signaling.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
RN [15]
RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1.
RX MEDLINE=21437805; PubMed=11553691;
RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
RT gamma-secretase is rapidly degraded but distributes partially in a
RT nuclear fraction of neurones in culture.";
RL J. Neurochem. 78:1168-1178(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions. Can promote transcription activation through binding
CC to APBB1/Tip60 and inhibit Notch signaling through interaction
CC with Numb. Couples to apoptosis-inducing pathways such as those
CC mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By
CC similarity). Acts as a kinesin I membrane receptor, mediating the
CC axonal transport of beta-secretase and presenilin 1. May be
CC involved in copper homeostasis/oxidative stress through copper ion
CC reduction. Can regulate neurite outgrowth through binding to
CC components of the extracellular matrix such as heparin and
CC collagen I and IV (By similarity). The splice isoforms that
CC contain the BPTI domain possess protease inhibitor activity (By
CC similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis.
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
CC its serine phosphorylation. Also interacts with GPCR-like protein
CC BPP, FPRL1, APPBP1, IB1, KNS2 (via its TPR domains), APPBP2 (via
CC BaSS) and DDB1 (By similarity). In vitro, it binds MAPT via the
CC MT-binding domains (By similarity). Associates with microtubules
CC in the presence of ATP and in a kinesin-dependent manner (By
CC similarity). Interacts, through a C-terminal domain, with GNAO1
CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 100.0%; Score 40; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KLVFFAED 8
              ||||||||
Db        687 KLVFFAED 694
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RESULT 11
A4_PIG
ID A4_PIG STANDARD; PRT; 770 AA.
AC P79307; Q29023; Q9TUI0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;

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RT   "Amyloid precursor protein 770.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-136 FROM N.A.
RC   TISSUE=Small intestine;
RA   Winteroe A.K., Fredholm M.;
RT   "Evaluation and characterization of a porcine small intestine cDNA
RT   library.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 667-723 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=92017079; PubMed=1656157;
RA   Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT   "Conservation of the sequence of the Alzheimer's disease amyloid
RT   peptide in dog, polar bear and five other mammals by cross-species
RT   polymerase chain reaction analysis.";
RL   Brain Res. Mol. Brain Res. 10:299-305(1991).
CC   -!- FUNCTION: Functions as a cell surface receptor and performs
CC       physiological functions on the surface of neurons relevant to
CC       neurite growth, neuronal adhesion and axonogenesis. Involved in
CC       cell mobility and transcription regulation through protein-protein
CC       interactions (By similarity). Can promote transcription activation
CC       through binding to APBB1/Tip60 and inhibit Notch signaling through
CC       interaction with Numb (By similarity). Couples to apoptosis-
CC       inducing pathways such as those mediated by G(O) and JIP (By
CC       similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC       Acts as a kinesin I membrane receptor, mediating the axonal
CC       transport of beta-secretase and presenilin 1 (By similarity). May
CC       be involved in copper homeostasis/oxidative stress through copper
CC       ion reduction (By similarity). In vitro, copper-metallated APP
CC       induces neuronal death directly or is potentiated through Cu(II)-
CC       mediated low-density lipoprotein oxidation (By similarity). Can
CC       regulate neurite outgrowth through binding to components of the
CC       extracellular matrix such as heparin and collagen I and IV (By
CC       similarity).
CC   -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC       with metal-reducing activity. Bind transient metals such as
CC       copper, zinc and iron (By similarity).
CC   -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC       peptides, including C31, are potent enhancers of neuronal
CC       apoptosis (By similarity).
CC   -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC       cytoplasmic proteins, including APBB family members, the APBA
CC       family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC       to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC       interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC       (via its TPR domains) (By similarity), APPBP2 (via BaSS) and DDB1.
CC       In vitro, it binds MAPT via the MT-binding domains (By
CC       similarity). Associates with microtubules in the presence of ATP
CC       and in a kinesin-dependent manner (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC       protein that rapidly becomes internalized via clathrin-coated
CC       pits. During maturation, the immature APP (N-glycosylated in the
CC       endoplasmic reticulum) moves to the Golgi complex where complete
CC       maturation occurs (O-glycosylated and sulfated). After alpha-
CC       secretase cleavage, soluble APP is released into the extracellular
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CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. Gamma-CTF(59) peptide is located to both the cytoplasm
CC and nuclei of neurons (By similarity).
CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gamma-CTF(50), gamma-CTF(57) and gamma-CTF(59) (By
CC similarity).
CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -!- SIMILARITY: Belongs to the APP family.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC --

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CC   ---------------------------------------------------------------------
DR   EMBL; AB032550; BAA84580.1; -.
DR   EMBL; Z84022; CAB06313.1; -.
DR   EMBL; X56127; CAA39592.1; -.
DR   HSSP; P05067; 1AAP.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW   Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
KW   Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW   Amyloid.
FT   SIGNAL        1     17       BY SIMILARITY.
FT   CHAIN        18    770       AMYLOID BETA A4 PROTEIN.
FT   CHAIN        18    687       SOLUBLE APP-ALPHA (POTENTIAL).
FT   CHAIN        18    671       SOLUBLE APP-BETA (POTENTIAL).
FT   CHAIN       672    770       C99 (BY SIMILARITY).
FT   CHAIN       672    713       BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT   CHAIN       672    711       BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT   CHAIN       688    770       C83 (BY SIMILARITY).
FT   CHAIN       688    713       P3(42) (BY SIMILARITY).
FT   CHAIN       688    711       P3(40) (BY SIMILARITY).
FT   CHAIN       712    770       GAMMA-CTF(59).
FT   CHAIN       714    770       GAMMA-CTF(57).
FT   CHAIN       721    770       GAMMA-CTF(50) (BY SIMILARITY).
FT   CHAIN       740    770       C31 (DURING APOPTOSIS) (BY SIMILARITY).
FT   DOMAIN       18    699       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    700    723       POTENTIAL.
FT   DOMAIN      724    770       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       96    110       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      135    155       COPPER-BINDING (BY SIMILARITY).
FT   DOMAIN      181    188       ZINC-BINDING (BY SIMILARITY).
FT   DOMAIN      291    341       BPTI/KUNITZ INHIBITOR.
FT   DOMAIN      391    423       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      491    522       HEPARIN-BINDING (BY SIMILARITY).
FT   DOMAIN      523    540       COLLAGEN-BINDING (BY SIMILARITY).
FT   DOMAIN      732    751       INTERACTION WITH G(O)-ALPHA (BY
FT                                 SIMILARITY).
FT   DOMAIN      230    260       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      274    280       POLY-THR.
FT   SITE        144    144       REQUIRED FOR COPPER(II) REDUCTION
FT                                 (BY SIMILARITY).
FT   ACT_SITE    301    302       REACTIVE BOND (BY SIMILARITY).
FT   SITE        671    672       CLEAVAGE (BY BETA-SECRETASE)
FT                                 (BY SIMILARITY).
FT   SITE        672    673       CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT   SITE        687    688       CLEAVAGE (BY ALPHA-SECRETASE)
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FT                                      (BY SIMILARITY).
FT   SITE        704    704             IMPLICATED IN FREE RADICAL PROPAGATION
FT                                      (BY SIMILARITY).
FT   SITE        706    706             INVOLVED IN OXIDATIVE REACTIONS
FT                                      (BY SIMILARITY).
FT   SITE        711    712             CLEAVAGE (BY GAMMA-SECRETASE; SITE 1)
FT                                      (BY SIMILARITY).
FT   SITE        713    714             CLEAVAGE (BY GAMMA-SECRETASE; SITE 2)
FT                                      (BY SIMILARITY).
FT   SITE        720    721             CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)

  Query Match             100.0%;  Score 40;  DB 1;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
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Db        687 KLVFFAED 694
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RESULT 12
A4_RAT
ID   A4_RAT          STANDARD;      PRT;   770 AA.
AC   P08592;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE   protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE   APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE   amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE   C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE   fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE   Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); C31].
GN   APP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM APP695).
RC   TISSUE=Brain;
RX   MEDLINE=88312583; PubMed=2900758;
RA   Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA   Seeburg P.H.;
RT   "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT   in rat brain suggests a role in cell contact.";
RL   EMBO J. 7:1365-1370(1988).
RN   [2]
RP   SEQUENCE OF 289-364 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89183625; PubMed=2648331;
RA   Kang J., Mueller-Hill B.;
RT   "The sequence of the two extra exons in rat preA4.";
RL   Nucleic Acids Res. 17:2130-2130(1989).
RN   [3]
RP   SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
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RX MEDLINE=21443797; PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=96187032; PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX MEDLINE=95263526; PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilineou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX MEDLINE=97150061; PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX MEDLINE=99127916; PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DDB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF 732-HIS-HIS-733.
RX MEDLINE=99162676; PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Go heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX MEDLINE=99316162; PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,

RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
RA Liu S.T., Howlett G., Barrow C.J.;
RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
RT of the A beta peptide of Alzheimer's disease.";
RL Biochemistry 38:9373-9378(1999).
RN [12]
RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
RP GLY-704.
RX MEDLINE=21956095; PubMed=11959460;
RA Kanski J., Varadarajan S., Aksenova M., Butterfield D.A.;
RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
RT peptide 1-42-associated oxidative stress and neurotoxicity.";
RL Biochim. Biophys. Acta 1586:190-198(2001).
RN [13]
RP PHOSPHORYLATION.
RX MEDLINE=97239592; PubMed=9085254;
RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
RA Greengard P., Suzuki T.;
RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
RT phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
RT cultured cells.";
RL Mol. Med. 3:111-123(1997).
RN [14]
RP PHOSPHORYLATION ON SER-730.
RX MEDLINE=99262094; PubMed=10329382;
RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
RA Greengard P., Nairn A.C., Suzuki T.;
RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
RT precursor protein at Ser655 by a novel protein kinase.";
RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
RN [15]
RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
RP THR-743.
RX MEDLINE=99274744; PubMed=10341243;
RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
RA Kirino Y., Greengard P., Suzuki T.;
RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
RT during neuronal differentiation.";
RL J. Neurosci. 19:4421-4427(1999).
RN [16]
RP PHOSPHORYLATION ON THR-743.
RX MEDLINE=20396183; PubMed=10936190;
RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
RT protein by cyclin-dependent kinase 5.";
RL J. Neurochem. 75:1085-1091(2000).
RN [17]
RP CARBOHYDRATE STRUCTURE OF APPICAN.
RX MEDLINE=21463085; PubMed=11479316;

RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
RA Sugahara K., Robakis N.K.;
RT "Appican, the proteoglycan form of the amyloid precursor protein,
RT contains chondroitin sulfate E in the repeating disaccharide region
RT and 4-O-sulfated galactose in the linkage region.";
RL J. Biol. Chem. 276:37155-37160(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP. Inhibits
CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
CC mediating the axonal transport of beta-secretase and presenilin 1
CC (By similarity). May be involved in copper homeostasis/oxidative
CC stress through copper ion reduction. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I and IV (By similarity). The
CC splice isoforms that contain the BPTI domain possess protease
CC inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
CC only weakly transient metals and have little reducing activity due
CC to substitutions of transient metal chelating residues. Beta-APP42
CC may activate mononuclear phagocytes in the brain and elicit
CC inflammatory responses. Promotes both tau aggregation and TPK II-
CC mediated phosphorylation (By similarity).
CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain.
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IB1, KNS2
CC (via its TPR domains), APPBP2 (via BaSS) (By similarity) and DDB1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity). Interacts,
CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
CC associates with HADH2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the

Query Match 100.0%; Score 40; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFAED 8

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                    ||||||||
Db          687 KLVFFAED 694


RESULT 13
A4_TETFL
ID   A4_TETFL       STANDARD;      PRT;   780 AA.
AC   O73683;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Tetraodon fluviatilis (Puffer fish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=47145;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF018165; AAC41275.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; 1.
DR   PROSITE; PS00320; A4_INTRA; 1.
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DR   PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    780       ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT                                 HOMOLOG.
FT   CHAIN       682    724       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    712    732       POTENTIAL.
FT   DOMAIN      733    780       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      323    382       BPTI/KUNITZ INHIBITOR.
FT   SITE        769    772       CLATHRIN-BINDING (BY SIMILARITY).
FT   DISULFID    327    378       BY SIMILARITY.
FT   DISULFID    336    361       BY SIMILARITY.
FT   CARBOHYD    560    560       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   780 AA;  88238 MW;  60071BE94520191D CRC64;

  Query Match             100.0%;  Score 40;  DB 1;  Length 780;
  Best Local Similarity   100.0%;  Pred. No. 0.38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||||||||
Db        697 KLVFFAED 704


RESULT 14
A4_FUGRU
ID   A4_FUGRU        STANDARD;      PRT;   737 AA.
AC   O93279;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE   Beta-amyloid protein (Beta-APP) (A-beta)].
GN   APP.
OS   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Takifugu.
OX   NCBI_TaxID=31033;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98252138; PubMed=9599080;
RA   Villard L., Tassone F., Crnogorac-Jurcevic T., Clancy K., Gardiner K.;
RT   "Analysis of pufferfish homologues of the AT-rich human APP gene.";
RL   Gene 210:17-24(1998).
CC   -!- FUNCTION: Functional neuronal receptor which couples to
CC       intracellular signaling pathway through the GTP-binding protein
CC       G(O) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the APP family.
CC   -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF090120; AAD13392.1; -.
DR   HSSP; P05067; 1HZ3.
DR   InterPro; IPR008155; A4_APP.
DR   InterPro; IPR008154; A4_extra.
DR   InterPro; IPR001255; Beta-APP.
DR   InterPro; IPR002223; Kunitz_BPTI.
DR   Pfam; PF02177; A4_EXTRA; 1.
DR   Pfam; PF03494; Beta-APP; 1.
DR   Pfam; PF00014; Kunitz_BPTI; 1.
DR   PRINTS; PR00203; AMYLOIDA4.
DR   PRINTS; PR00759; BASICPTASE.
DR   ProDom; PD000222; Kunitz_BPTI; 1.
DR   SMART; SM00006; A4_EXTRA; 1.
DR   SMART; SM00131; KU; 1.
DR   PROSITE; PS00319; A4_EXTRA; FALSE_NEG.
DR   PROSITE; PS00320; A4_INTRA; 1.
DR   PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR   PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW   Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW   Serine protease inhibitor.
FT   SIGNAL        1     18       POTENTIAL.
FT   CHAIN        19    737       ALZHEIMER'S DISEASE AMYLOID A4
FT                                 PROTEIN HOMOLOG.
FT   CHAIN       639    681       BETA-AMYLOID PROTEIN (POTENTIAL).
FT   DOMAIN       19    668       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    669    689       POTENTIAL.
FT   DOMAIN      690    737       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      286    344       BPTI/KUNITZ INHIBITOR.
FT   SITE        726    729       CLATHRIN-BINDING (BY SIMILARITY).
FT   ACT_SITE    300    301       REACTIVE BOND.
FT   DISULFID    290    340       BY SIMILARITY.
FT   DISULFID    299    323       BY SIMILARITY.
FT   DISULFID    315    336       BY SIMILARITY.
FT   CARBOHYD    522    522       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   737 AA;  82856 MW;  6FAD01E2E3B2B7E2 CRC64;

  Query Match             92.5%;  Score 37;  DB 1;  Length 737;
  Best Local Similarity   87.5%;  Pred. No. 1.7;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              |||||||:|
Db        654 KLVFFADD 661


RESULT 15
Y189_RICPR
ID   Y189_RICPR     STANDARD;      PRT;   321 AA.
AC   Q9ZDX5;
DT   30-MAY-2000 (Rel. 39, Created)
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DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein RP189.
GN   RP189.
OS   Rickettsia prowazekii.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Rickettsieae; Rickettsia.
OX   NCBI_TaxID=782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Madrid E;
RX   MEDLINE=99039499; PubMed=9823893;
RA   Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA   Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA   Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT   "The genome sequence of Rickettsia prowazekii and the origin of
RT   mitochondria.";
RL   Nature 396:133-140(1998).
CC   -!- SIMILARITY: SOME, TO A.AEOLICUS AQ_1104.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ235270; CAA14655.1; -.
DR   PIR; H71729; H71729.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   321 AA;  36653 MW;  3E5F47D104DD8A73 CRC64;

  Query Match             85.0%;  Score 34;  DB 1;  Length 321;
  Best Local Similarity   75.0%;  Pred. No. 3.7;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KLVFFAED 8
              ||:|||  |
Db        178 KLIFFAHD 185


Search completed: March  4, 2004, 15:36:26
Job time : 1.25532 secs
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